

FIGURE 1

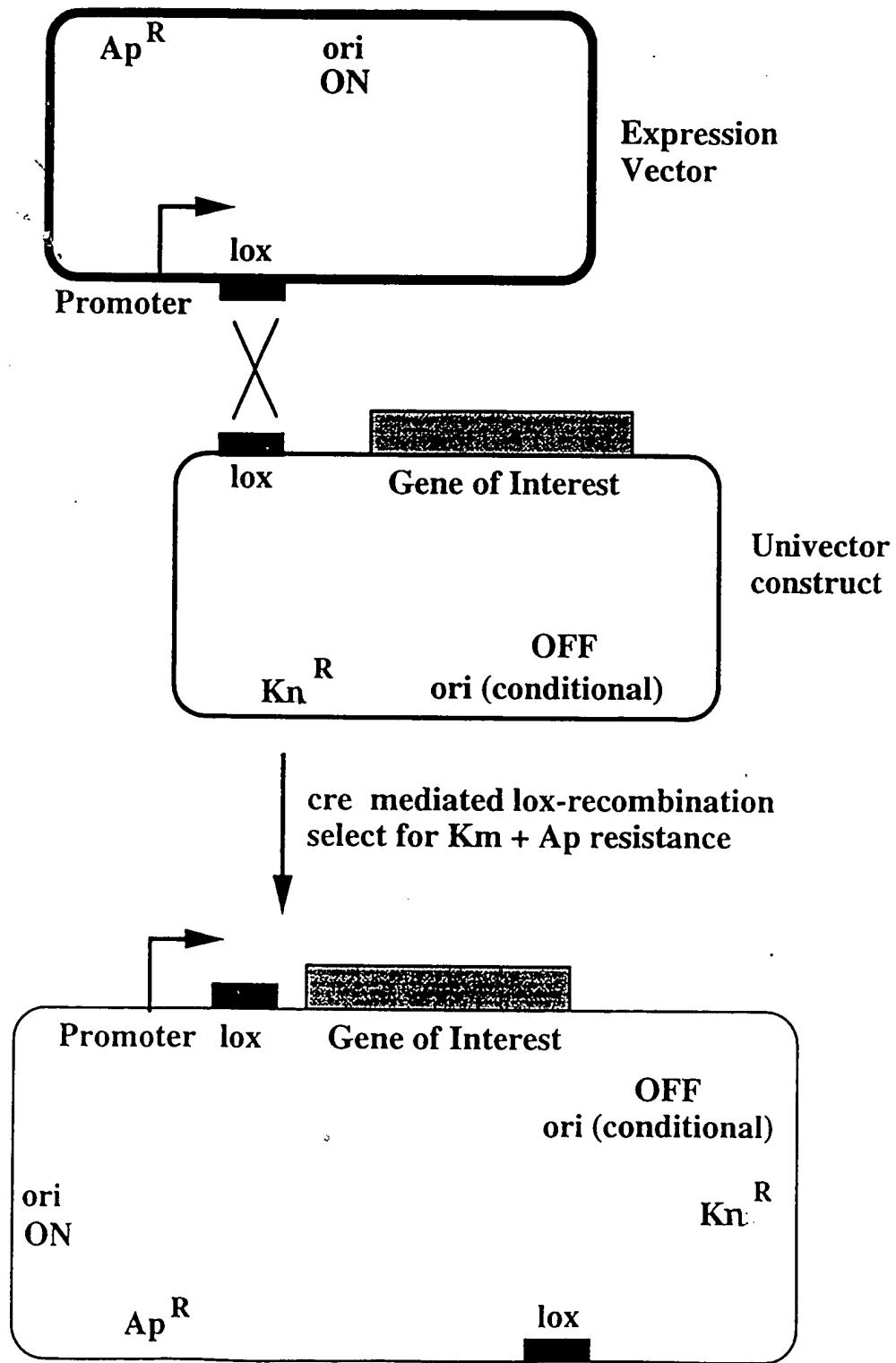
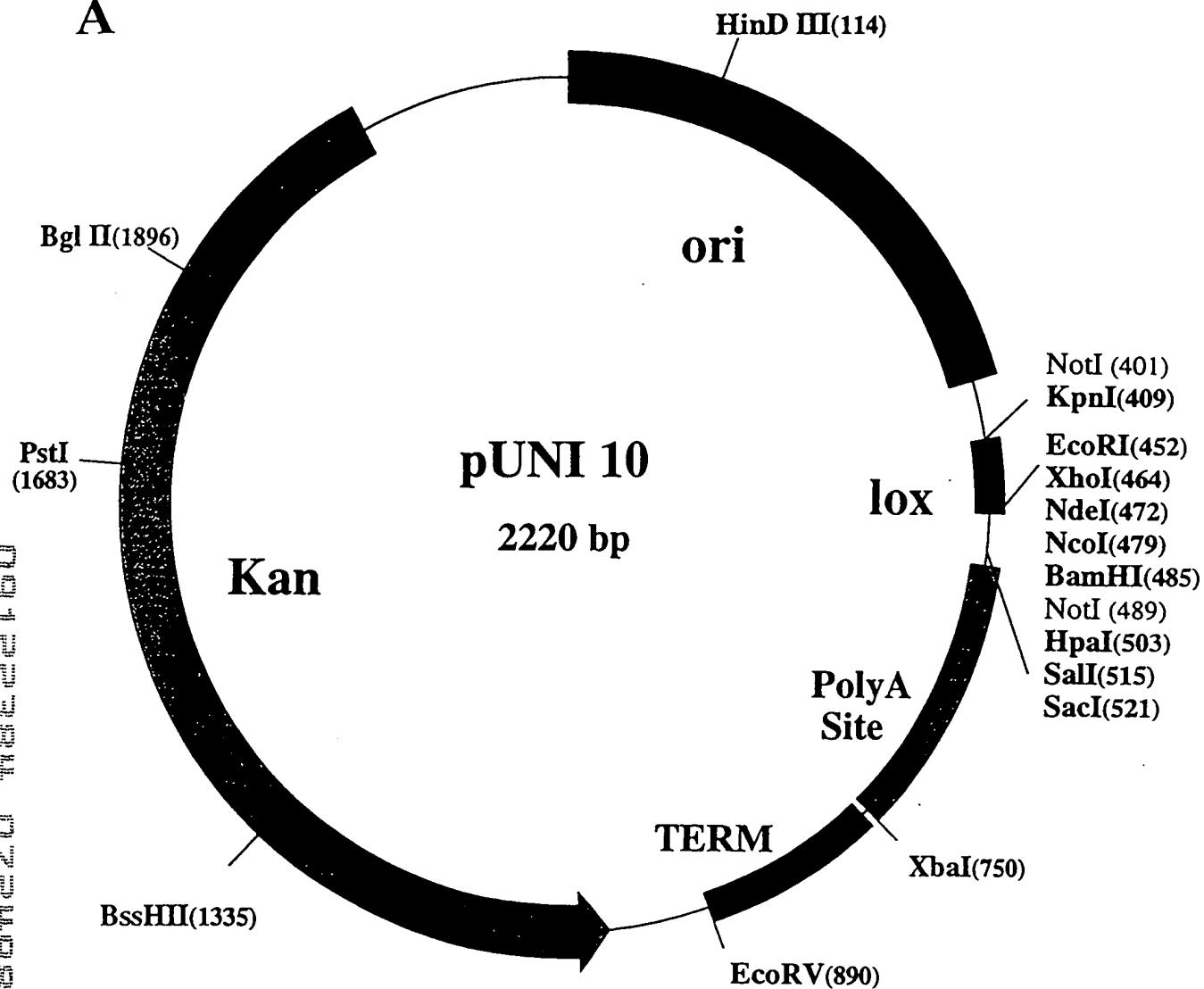


FIGURE 2

A



B

<u>(401) NotI</u>	<u>KpnI</u>	<u>LOX</u>				
GC GGC CGC GGT ACC ATA ACT TCG TAT AGC ATA CAT TAT ACG AAG TTA TCT						
<u>EcoRI</u>	<u>SmaI</u>	<u>XhoI</u>	<u>NdeI</u>	<u>NcoI</u>	<u>BamHI</u>	<u>NotI</u>
GGA ATT CCC CGG GCT CGA GAA CAT ATG GCC ATG GGG ATC CGC GGC CGC						
<u>HpaI</u>	<u>Sall</u>	<u>SacI</u>				
AAT TGT TAA CAG ATC CGT CGA CGA GCT CGC TA (530)						

## FIGURE 3

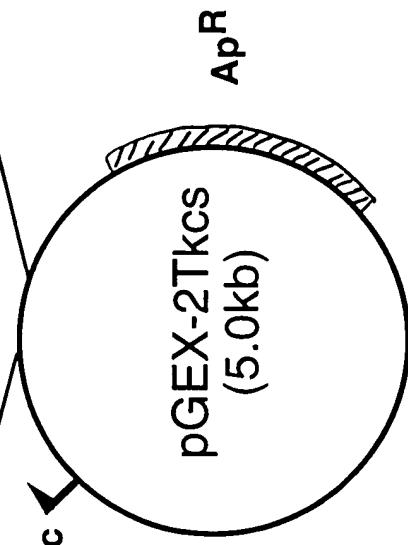
### Construction of pGst-lox:

A

Linker: C ATG GCT ATA ACT TCG TAT AGC ATA CAT TAT ACG AAG TTA TG  
CGA TAT TGA AGC ATA TCG TAT GTA ATA TGC TTC AAT AC CTTA  
NcoI BamHI

B

MCS: CAT ATG CCC ATG GCT CGA GGA TCC GAA TTC  
NdeI NcoI BamHI



## FIGURE 4

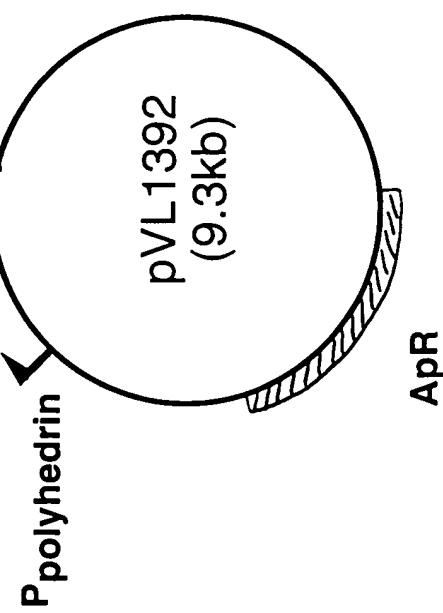
### Construction of pVL1392-10X:

**A**

Linker: GG CCG GAC GTC ATA ACT TCG TAT AGC ATA CAT TAT ACG AAG TTA TG  
C CTG CAG TAT TGA AGC ATA TCG TAT GTA ATA TGC TTC AAT AC CTTAG  
**NotI** **BamHI**

**B**

MCS: BglII/PstI/**NotI**/XmaI/ECORI/XbaI/SmaI/**BamHI**



Construction of pGAP24-lox:

A

Linker: T.CGA GAC GTC ATA ACT TCG TAT AGC ATA CAT TAT ACG AAG TTA TGC  
CTG CAG TAT TGA AGC ATA TCG TAT GTA ATA TGC TAT AAT ACG CCGG  
XbaI NotI

B

MCS: **Xba**I/**Bcl**II/**Not**I/**Eag**I/**Sty**I/**Afl**III

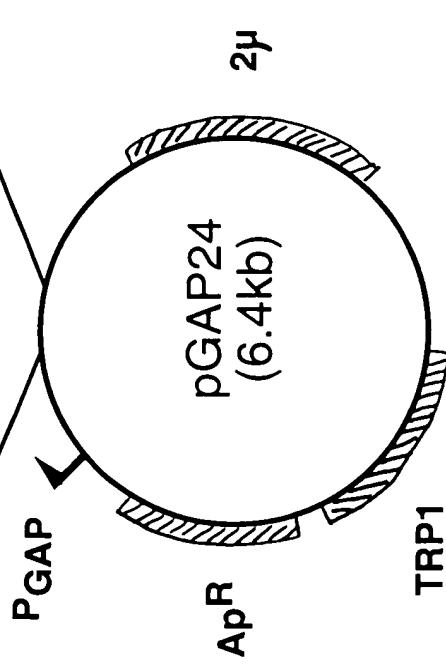


FIGURE 6

Construction of pGAL14-1ox:

A

Linker: T CGA GAC GTC ATA ACT TCG TAT AGC ATA CAT TAT ACG AAG TTA TGC  
CTG CAG TAT TGA AGC ATA TCG TAT GTA ATA TGC TTC ATT ACG CCGG  
XbaI NotI

B

MCS: SalI/ClaI/PstI/SmaI/XbaI/SpeI/NotI/EagI/SacII/SacI

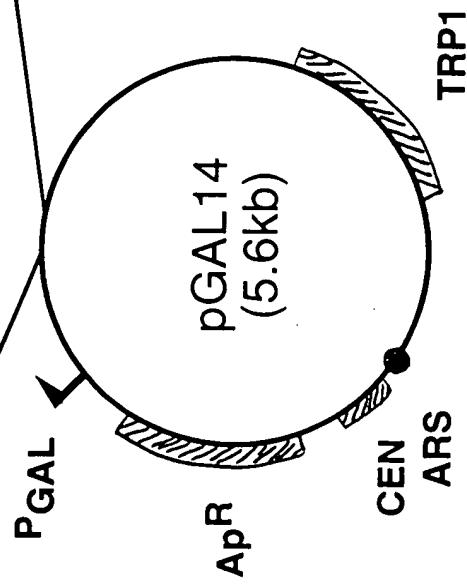


FIGURE 7

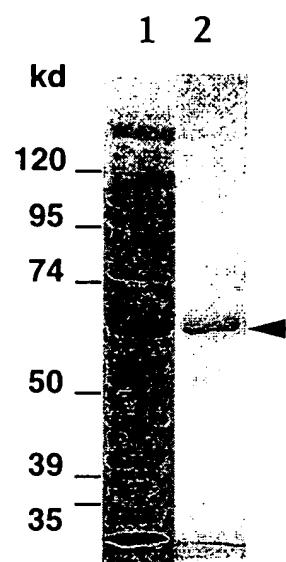


FIGURE 8

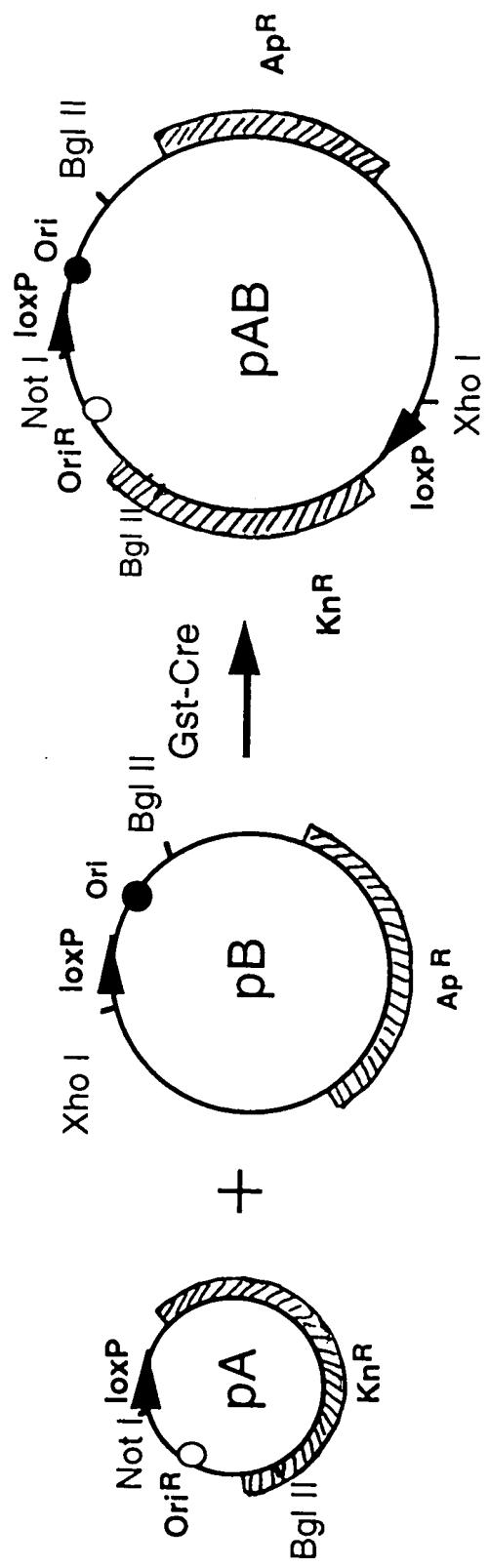
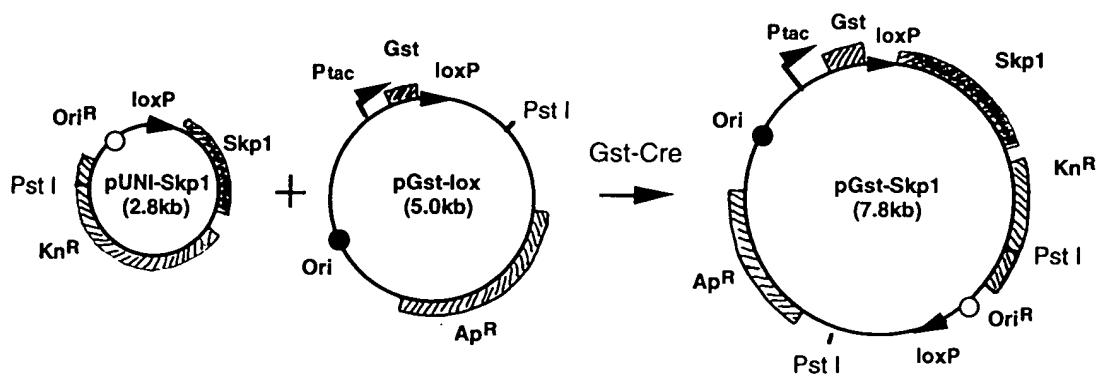


FIGURE 9

A



B

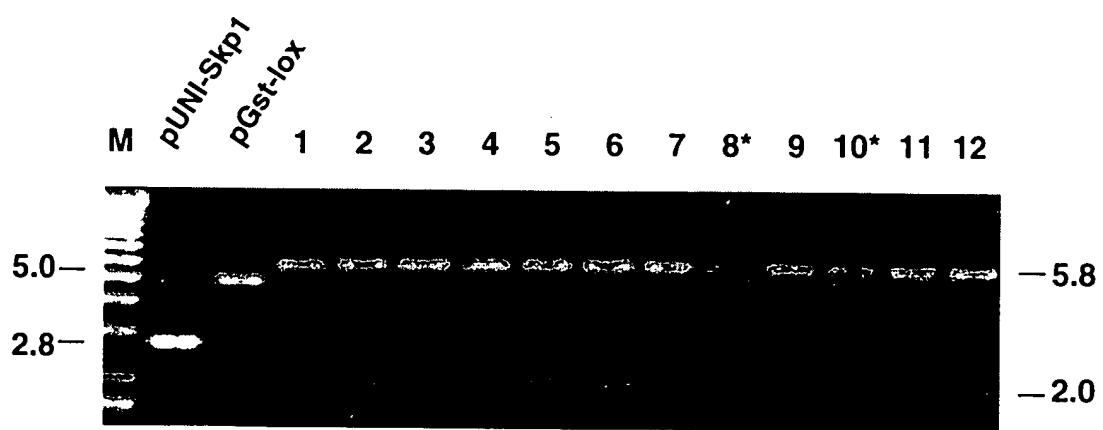
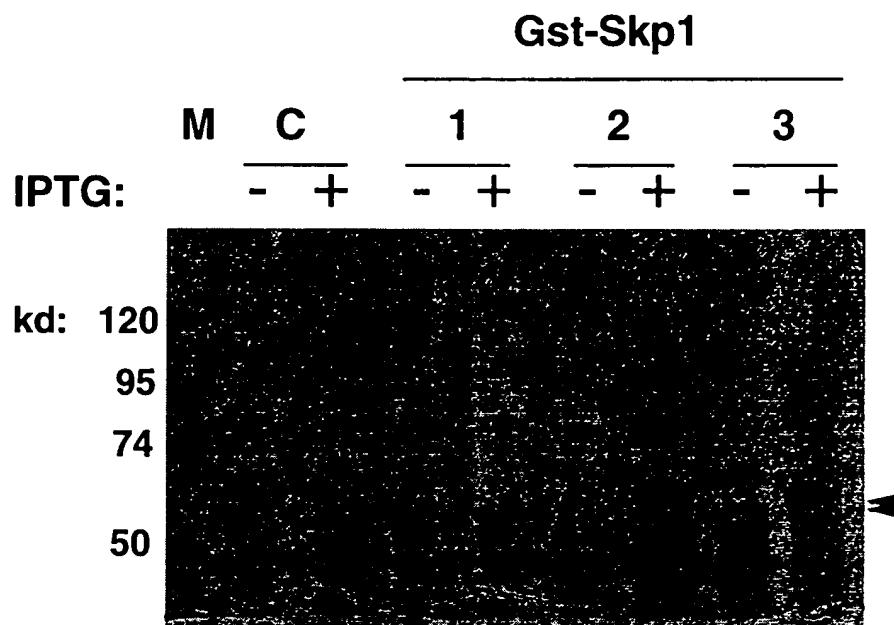
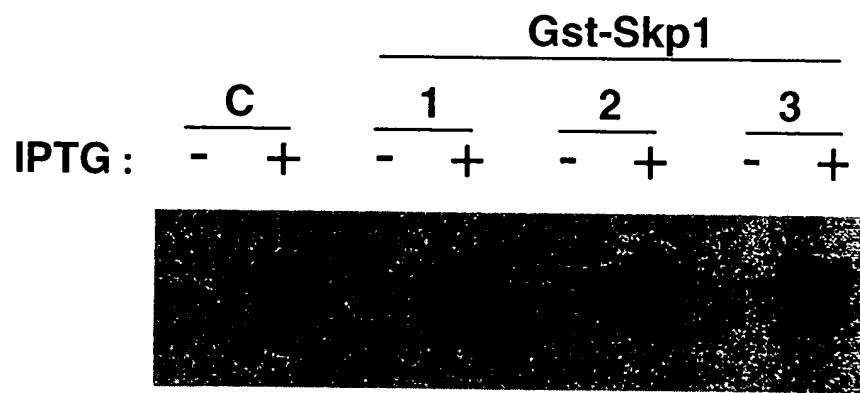


FIGURE 10

A



B



## FIGURE 11

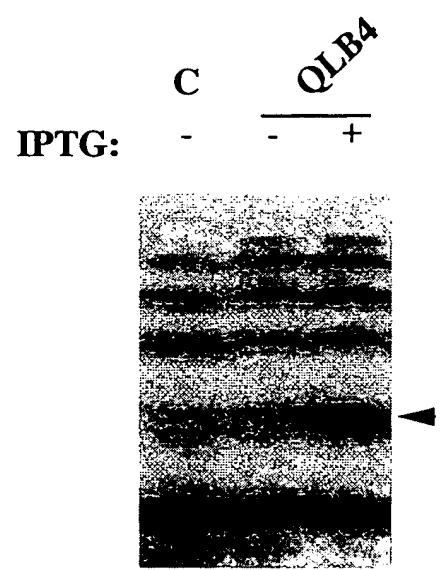
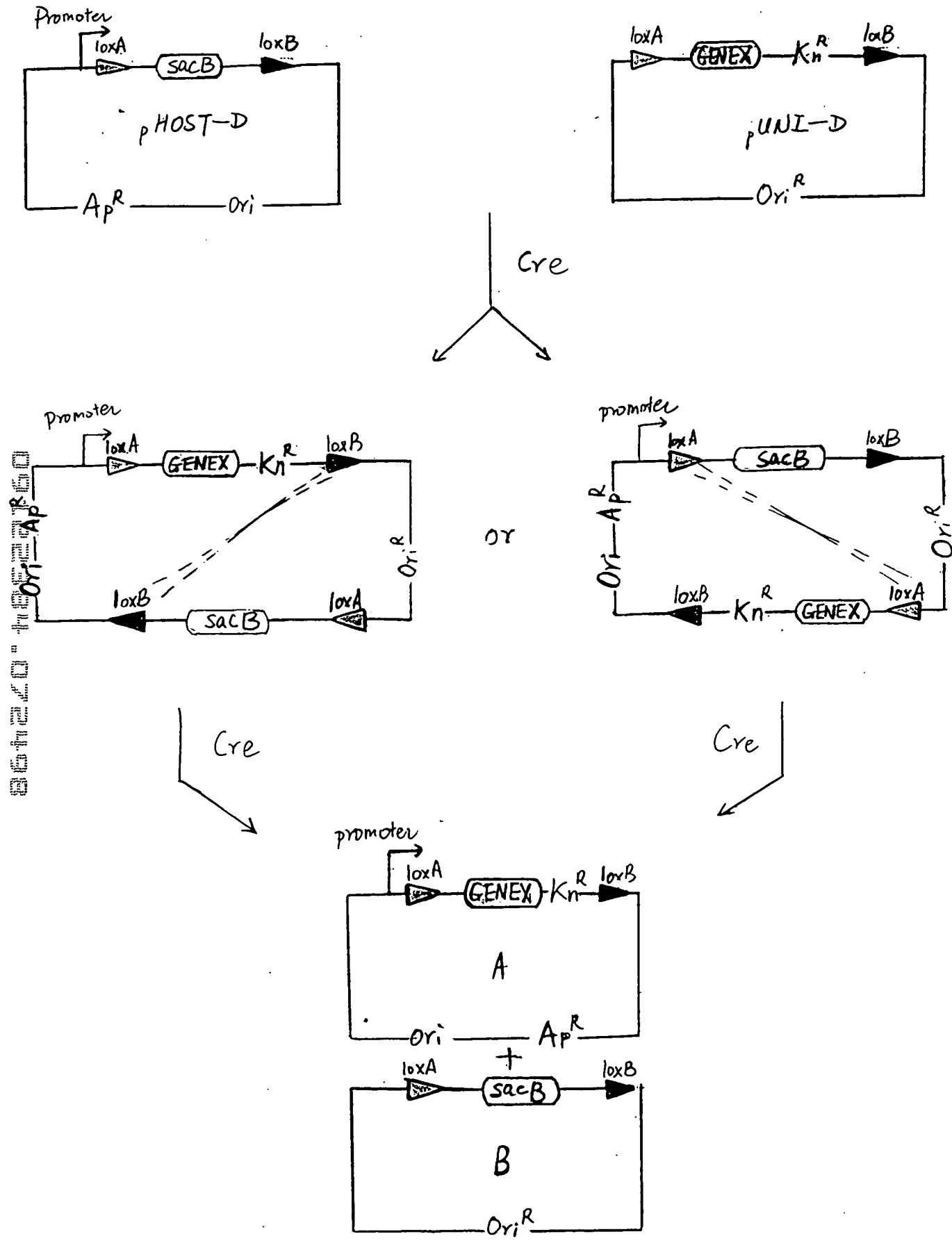


FIGURE 12



## FIGURE 13

loxP:

ATAACTTCGTATA GCATACAT TATA CGAAGTTAT  
1 2 3 4 5 6 7 8 9 10 11 12 13 13 12 11 10 9 8 7 6 5 4 3 2 1

T C

loxP2:

ATAACTTCGTATA GCATACAT TATA CGAAGTTAT  
1 2 3 4 5 6 7 8 9 10 11 12 13 13 12 11 10 9 8 7 6 5 4 3 2 1

T

loxP3:

ATAACTTCGTATA GCATACAT TATA CGAAGTTAT  
1 2 3 4 5 6 7 8 9 10 11 12 13 13 12 11 10 9 8 7 6 5 4 3 2 1

T C

loxP23

ATAACTTCGTATA GCATACAT TATA CGAAGTTAT  
1 2 3 4 5 6 7 8 9 10 11 12 13 13 12 11 10 9 8 7 6 5 4 3 2 1

FIGURE 14

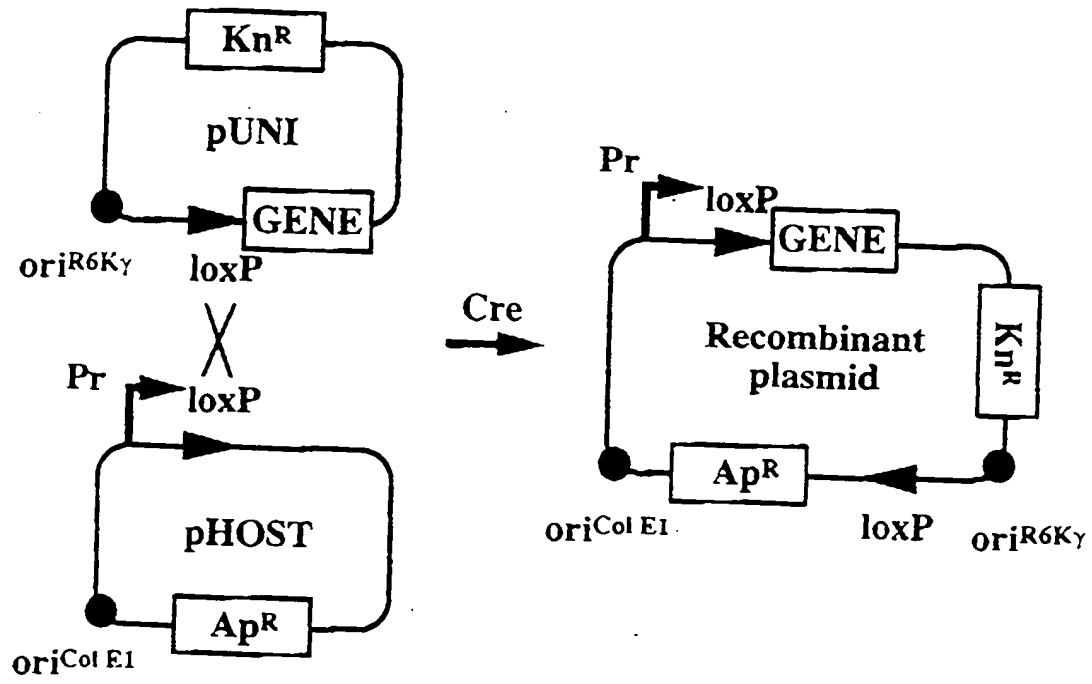


FIGURE 15

GST-Cre (μg)	number of Ap <sup>R</sup> transformants	number of Kn <sup>R</sup> transformants	Kn <sup>R</sup> /Ap <sup>R</sup> (%)
0	4.0 x 10 <sup>5</sup>	0	0
0.02	3.0 x 10 <sup>5</sup>	231	0.1
0.04	2.3 x 10 <sup>5</sup>	406	0.2
0.06	2.4 x 10 <sup>5</sup>	868	0.4
0.08	3.3 x 10 <sup>5</sup>	1,336	0.4
0.10	6.0 x 10 <sup>4</sup>	594	1.0
0.20	7.8 x 10 <sup>4</sup>	580	0.7
0.40	5.8 x 10 <sup>4</sup>	1,910	3.3
0.60	9.2 x 10 <sup>4</sup>	10,750	11.7
0.80	3.1 x 10 <sup>5</sup>	28,660	9.2
1.00	1.0 x 10 <sup>5</sup>	16,840	16.8

FIGURE 16

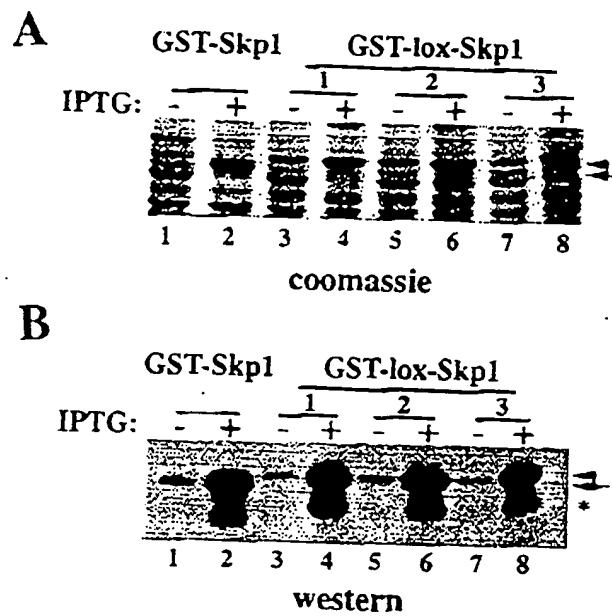


FIGURE 17

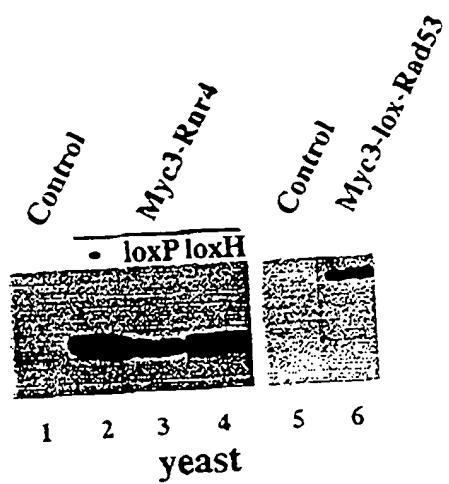
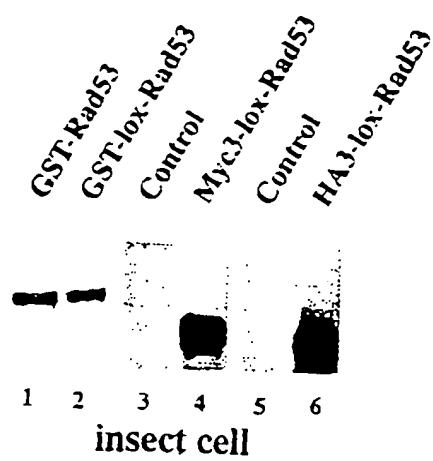


FIGURE 18



7  
**FIGURE 19**

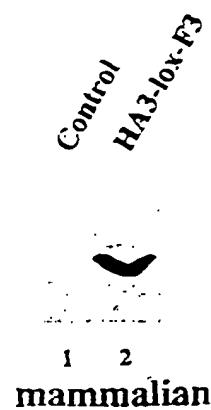


FIGURE 20

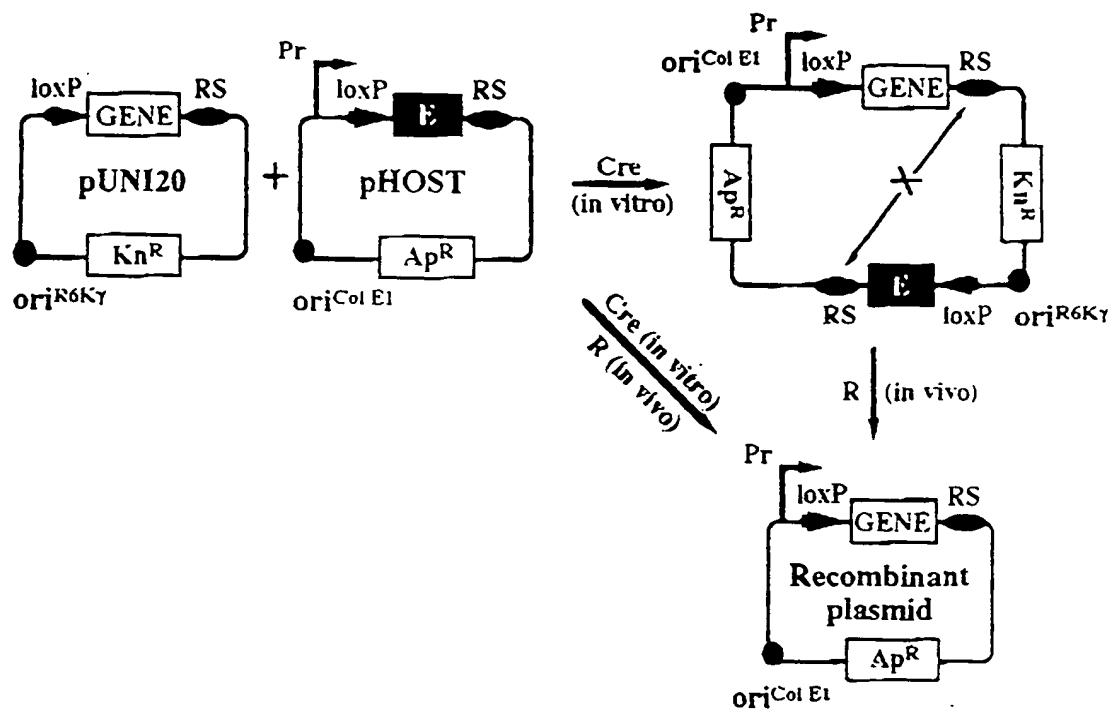


FIGURE 21

Pvu II restriction analysis of recombinant  
plasmids made by one-step POT

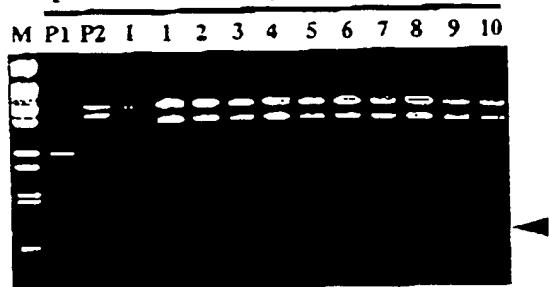


FIGURE 22

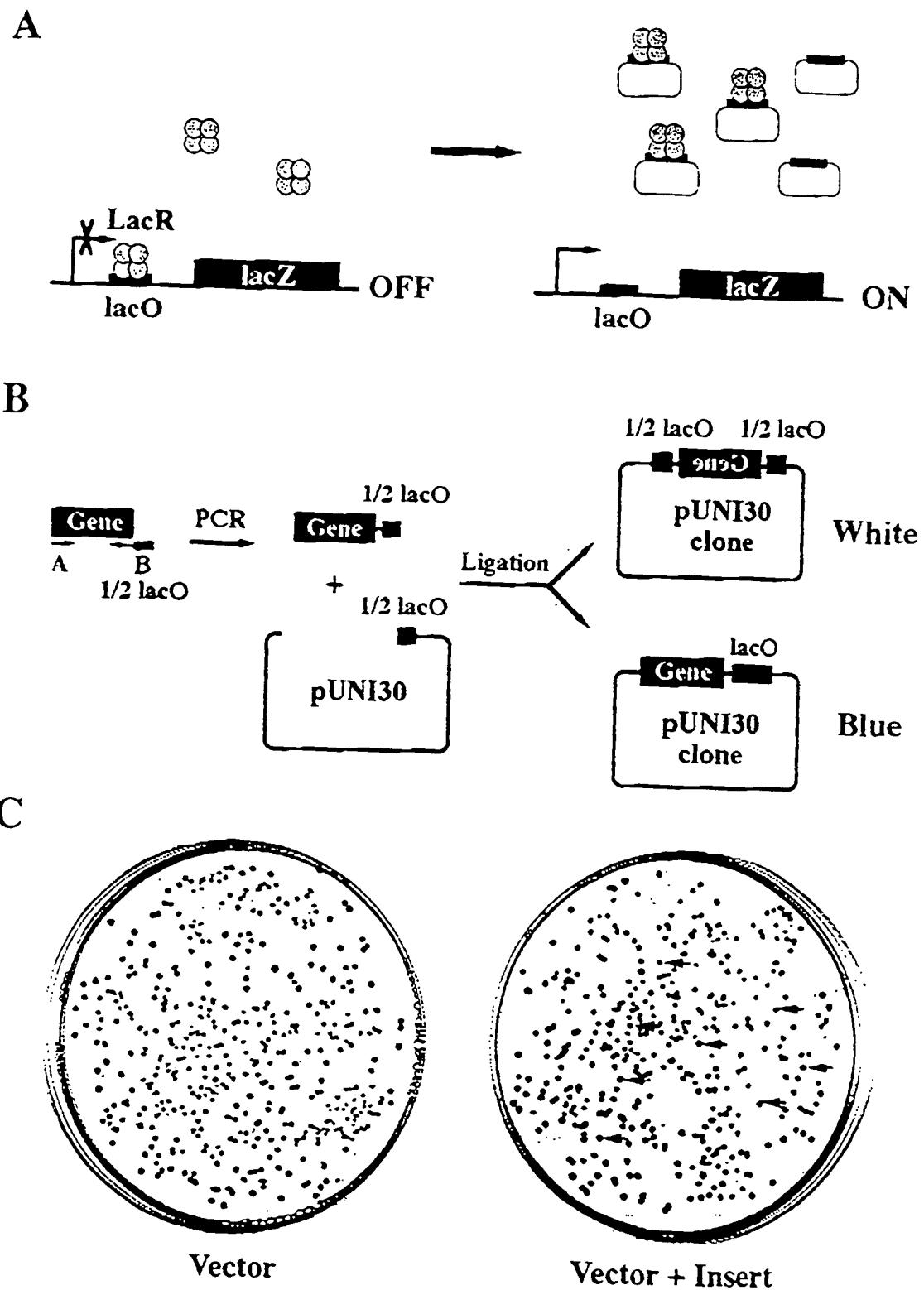
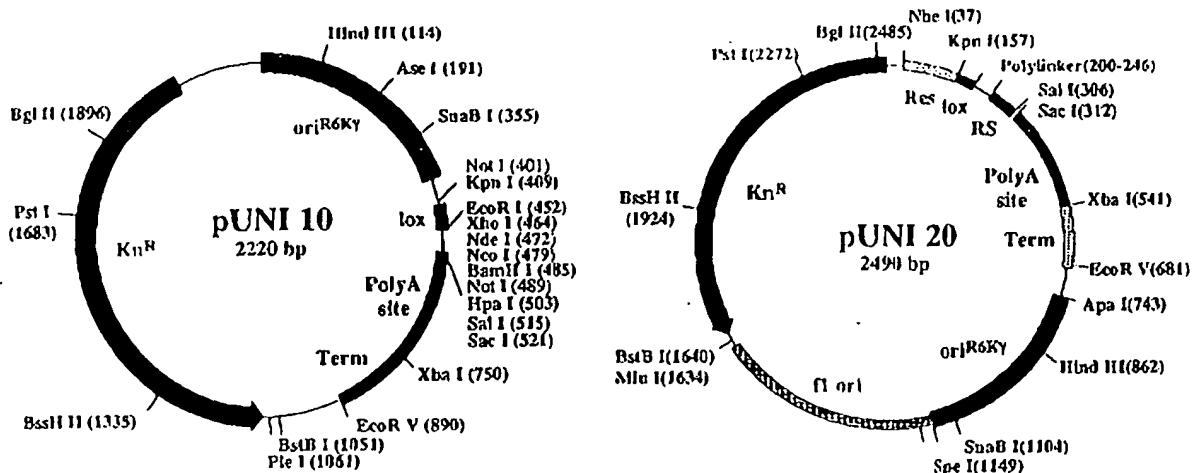


FIGURE 23



pUNI 10 Polylinker Sequence

(401) Not I KpnI LOX

GC CGC CGC GGT ACC ATA ACT TCG TAT AGC ATA CAT TAT ACG A

AG TTA TCT GGA ATT CCC CGG GCT CGA GAA CAT ATG GCC ATG G

EcoR I Sma I Xba I Nde I Nco I

GG ATC CGC GGC CGC AAT TGT TAA CAG ATC CGT CGA CGA GCT

BamH I Not I Hpa I Sal I Sac I (530)

GG ATC CGC GGC CGC AAT TGT TAA CAG ATC CGT CGA CGA GCT

pUNI 20 Polylinker Sequence

(157) KpnI LOX

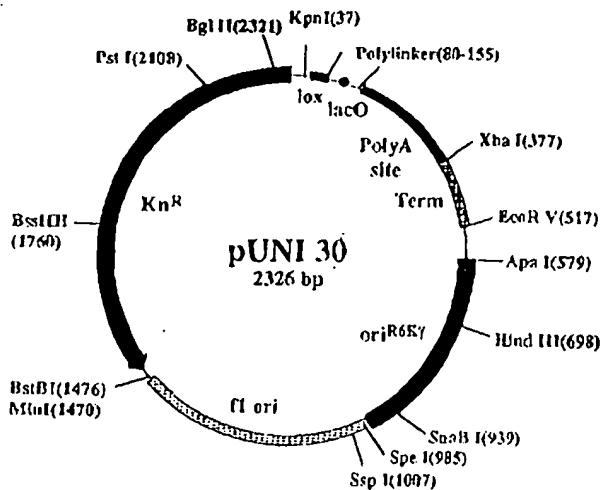
GGT ACC ATA ACT TCG TAT AGC ATA CAT TAT ACG AAG TTA T

EcoR I Sma I Xba I Nde I Nco I BsaH III

CT GGA ATT CCC CGG GCT CGA GAA CAT ATG GCC ATG CGC ATC

Not I (246)

CGC GGC CGC



pUNI 30 Polylinker Sequence

(37) KpnI LOX

GGT ACC ATA ACT TCG TAT AGC ATA CAT TAT ACG AAG TTA T

EcoR I Sma I Xba I EcoRIII

T GGA ATT CCC CGG GCT CGA GCC AGT CCA CGG CTC ACA ATT

half lacO

Not I Hpa I Sal I Sac I (155)

GGC GCC CGA ATT GTT AAC AGA TCC GTC GAC GAG CTC GC

MnlI

FIGURE 24

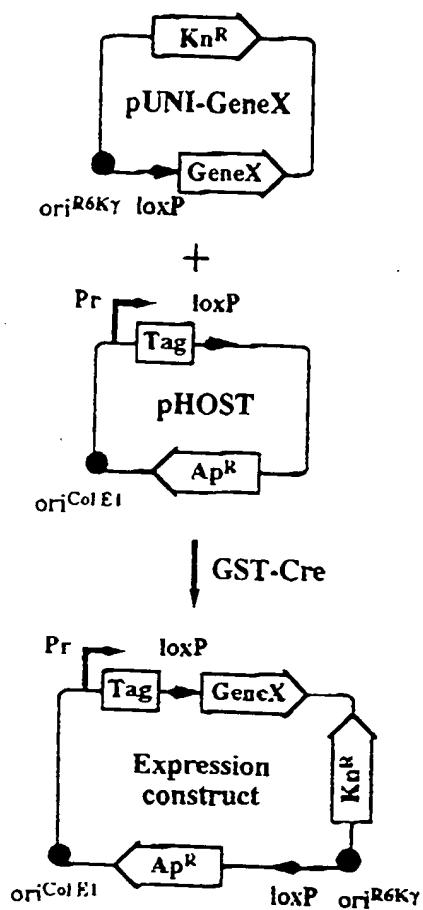
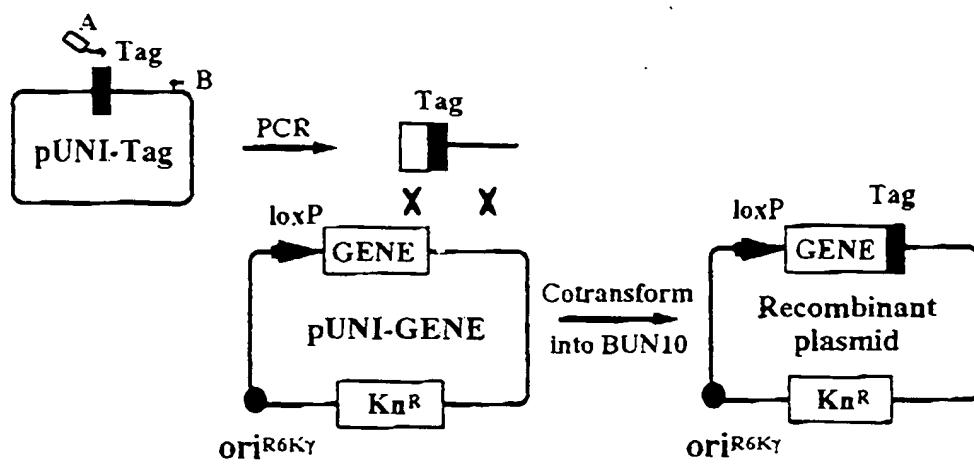


FIGURE 25



## FIGURE 26A

SEQUENCE DESCRIPTION: SEQ ID NO:1:

AATTCTGTCA GCCGTTAAGT GTTCCTGTGT CACTGAAAAT TGCTTGAGA GGCTCTAAGG  
60

GCTTCTCAGT GCGTTACATC CCTGGCTTGT TGTCCACAAC CGTTAAACCT TAAAAGCTTT  
120

AAAAGCCTTA TATATTCTTT TTTTCTTAT AAAACTTAAA ACCTTAGAGG CTATTTAAGT  
180

TGCTGATTAA TATTAATTAA ATTGTTCAAA CATGAGAGCT TAGTACGTGA AACATGAGAG  
240

CTTAGTACGT TAGCCATGAG AGCTTAGTAC GTTAGCCATG AGGGTTAGT TCGTTAAACA  
300

TGAGAGCTTA GTACGTTAAA CATGAGAGCT TAGTACGTGA AACATGAGAG CTTAGTACGT  
360

ACTATCAACA GGTGAACTG CTGATCAACA GATCCTCTAC GCGGCCGCGG TACCATAACT  
420

TCGTATAGCA TACATTATAC GAAGTTATCT GGAATTCCCC GGGCTCGAGA ACATATGGCC  
480

ATGGGGATCC GCGGCCGCAA TTGTTAACAG ATCCGTCGAC GAGCTCGCTA TCAGCCTCGA  
540

CTGTGCCTTC TAGTTGCCAG CCATCTGTTG TTTGCCCTC CCCCCTGCCT TCCTTGACCC  
600

TGGAAGGTGC CACTCCCACT GTCCTTCCT AATAAAATGA GGAAATTGCA TCGCATTGTC  
660

TGAGTAGGTG TCATTCTATT CTGGGGGGTG GGGTGGGGCA GGACAGCAAG GGGGAGGATT  
720

GGGAAGACAA TAGCAGGCAT GCTGGGGATT CTAGAAGATC CGGCTGCTAA CAAAGCCGA  
780

AAGGAAGCTG AGTTGGCTGC TGCCACCGCT GAGCAATAAC TAGCATAACC CCTTGGGGCC  
840

TCTAACCGGG TCTTGAGGGG TTTTTGCTG AAAGGAGGAA CTATATCCGG ATATCCGGG  
900

GTGGGCGAAG AACTCCAGCA TGAGATCCCC GCGCTGGAGG ATCATCCAGC CGGCGTCCCG  
960

AAAAACGATT CCGAAGCCCA ACCTTCATA GAAGGCGGCG GTGGAATCGA AATCTCGTGA  
1020

TGGCAGGTTG GGCGTCGCTT GGTGGTCAT TTGAAACCCC AGAGTCCCGC TCAGAAGAAC  
1080

TCGTCAAGAA GGCGATAGAA GGCGATGCGC TGCGAATCGG GAGCGGCGAT ACCGTAAGC  
1140

ACGAGGAAGC GGTCAGGCCA TTGCGCGCCA AGCTCTTCAG CAATATCACG GGTAGCCAAC  
1200

GCTATGTCTT GATAGCGGTC CGCCACACCC AGCCGGCCAC AGTCGATGAA TCCAGAAAAG  
1260

CGGCCATTTC CCACCATGAT ATTGGCAAG CAGGCATCGC CATGGGTAC GACGAGATCC  
1320

TCGCCGTCGG GCATGCGCGC CTTGAGCCTG GCGAACAGTT CGGCTGGCGC GAGCCCCTGA  
1380

TGCTCTTCGT CCAGATCATC CTGATCGACA AGACCGGCTT CCATCCGAGT ACGTGCTCGC  
1440

TCGATGCGAT GTTCGCTTG GTGGTCGAAT GGGCAGGTAG CCGGATCAAG CGTATGCAGC  
1500

CGCCGCATTG CATCAGCCAT GATGGATACT TTCTCGGCAG GAGCAAGGTG AGATGACAGG  
1560

AGATCCTGCC CCGGCACCTTC GCCCAATAGC AGCCAGTCCC TTCCCGCTTC AGTGACAAACG  
1620

TCGAGCACAG CTGCGCAAGG AACGCCCGTC GTGGCCAGCC ACGATAGCCG CGCTGCCTCG  
1680

TCCTGCAGTT CATTCAAGGC ACCGGACAGG TCGGTCTTGA CAAAAAGAAC CGGGCGCCCC  
1740

TGCGCTGACA GCCGGAACAC GGCGGCATCA GAGCAGCCGA TTGTCTGTTG TGCCCAGTCA  
1800

TAGCCGAATA GCCTCTCCAC CCAAGCGGCC GGAGAACCTG CGTGAATCC ATCTTGTCA  
1860

ATCATGCGAA ACGATCCTCA TCCTGTCTCT TGATCAGATC TTGATCCCCT GCGCCATCAG  
1920

ATCCTTGGCG GCAAGAAAGC CATCCAGTTT ACTTTGCAGG GCTTCCCAAC CTTACCAGAG  
1980

GGCGCCCCAG CTGGCAATTG CGGTTGCGTT GCTGTCCATA AAACCGCCCA GTCTAGCTAT  
2040

GCCCATGTAA GCCCACTGCA AGCTACCTGC TTTCTCTTG CGCTTGCAGTT TTCCCTTGTC  
2100

CAGATAGCCC AGTAGCTGAC ATTCACTCCGG GGTCAGCACC GTTTCTGCGG ACTGGCTTC  
2160

TACGTGTTCC GCTTCCTTTA GCAGCCCTTG CGCCCTGAGT GCTTGCGGCA GCGTGAAGCT  
2220

## FIGURE 26B

SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG TCC CCT ATA CTA GGT TAT TGG AAA ATT AAG GGC CTT GTG CAA CCC  
48

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
1 5 10 15

ACT CGA CTT CTT TTG GAA TAT CTT GAA GAA AAA TAT GAA GAG CAT TTG  
96

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
20 25 30

TAT GAG CGC GAT GAA GGT GAT AAA TGG CGA AAC AAA AAG TTT GAA TTG  
144

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
35 40 45

GGT TTG GAG TTT CCC AAT CTT CCT TAT TAT ATT GAT GGT GAT GTT AAA  
192

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
50 55 60

TTA ACA CAG TCT ATG GCC ATC ATA CGT TAT ATA GCT GAC AAG CAC AAC  
240

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
65 70 75 80

ATG TTG GGT GGT TGT CCA AAA GAG CGT GCA GAG ATT TCA ATG CTT GAA  
288

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
85 90 95

GGA GCG GTT TTG GAT ATT AGA TAC GGT GTT TCG AGA ATT GCA TAT AGT  
336

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
100 105 110

AAA GAC TTT GAA ACT CTC AAA GTT GAT TTT CTT AGC AAG CTA CCT GAA  
384

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
115 120 125

ATG CTG AAA ATG TTC GAA GAT CGT TTA TGT CAT AAA ACA TAT TTA AAT  
432

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
130 135 140

GGT GAT CAT GTA ACC CAT CCT GAC TTC ATG TTG TAT GAC GCT CTT GAT  
480

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
145 150 155 160

GTT GTT TTA TAC ATG GAC CCA ATG TGC CTG GAT GCG TTC CCA AAA TTA  
528  
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
165 170 175

GTT TGT TTT AAA AAA CGT ATT GAA GCT ATC CCA CAA ATT GAT AAG TAC  
576  
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
180 185 190

TTG AAA TCC AGC AAG TAT ATA GCA TGG CCT TTG CAG GGC TGG CAA GCC  
624  
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
195 200 205

ACG TTT GGT GGT GGC GAC CAT CCT CCA AAA TCG GAT CTG GTT CCG CGT  
672  
Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
210 215 220

GGA TCT CGT CGT GCA TCT GTT GGA TCG CAT ATG CCC ATG GCC AAT TTA  
720  
Gly Ser Arg Arg Ala Ser Val Gly Ser His Met Pro Met Ala Asn Leu  
225 230 235 240

CTG ACC GTA CAC CAA AAT TTG CCT GCA TTA CCG GTC GAT GCA ACG AGT  
768  
Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val Asp Ala Thr Ser  
245 250 255

GAT GAG GTT CGC AAG AAC CTG ATG GAC ATG TTC AGG GAT CGC CAG GCG  
816  
Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg Asp Arg Gln Ala  
260 265 270

TTT TCT GAG CAT ACC TGG AAA ATG CTT CTG TCC GTT TGC CGG TCG TGG  
864  
Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val Cys Arg Ser Trp  
275 280 285

GCG GCA TGG TGC AAG TTG AAT AAC CGG AAA TGG TTT CCC GCA GAA CCT  
912  
Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe Pro Ala Glu Pro  
290 295 300

GAA GAT GTT CGC GAT TAT CTT CTA TAT CTT CAG GCG CGC GGT CTG GCA  
960  
Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala Arg Gly Leu Ala  
305 310 315 320

GTA AAA ACT ATC CAG CAA CAT TTG GGC CAG CTA AAC ATG CTT CAT CGT  
1008  
Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn Met Leu His Arg  
325 330 335

CGG TCC GGG CTG CCA CGA CCA AGT GAC AGC AAT GCT GTT TCA CTG GTT  
1056  
Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala Val Ser Leu Val  
340 345 350

ATG CGG CGG ATC CGA AAA GAA AAC GTT GAT GCC GGT GAA CGT GCA AAA  
1104  
Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly Glu Arg Ala Lys  
355 360 365

CAG GCT CTA GCG TTC GAA CGC ACT GAT TTC GAC CAG GTT CGT TCA CTC  
1152  
Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln Val Arg Ser Leu  
370 375 380

ATG GAA AAT AGC GAT CGC TGC CAG GAT ATA CGT AAT CTG GCA TTT CTG  
1200  
Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn Leu Ala Phe Leu  
385 390 395 400

GGG ATT GCT TAT AAC ACC CTG TTA CGT ATA GCC GAA ATT GCC AGG ATC  
1248  
Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu Ile Ala Arg Ile  
405 410 415

AGG GTT AAA GAT ATC TCA CGT ACT GAC GGT GGG AGA ATG TTA ATC CAT  
1296  
Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg Met Leu Ile His  
420 425 430

ATT GGC AGA ACG AAA ACG CTG GTT AGC ACC GCA GGT GTA GAG AAG GCA  
1344  
Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly Val Glu Lys Ala  
435 440 445

CTT AGC CTG GGG GTA ACT AAA CTG GTC GAG CGA TGG ATT TCC GTC TCT  
1392  
Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp Ile Ser Val Ser  
450 455 460

GGT GTA GCT GAT GAT CCG AAT AAC TAC CTG TTT TGC CGG GTC AGA AAA  
1440  
Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys Arg Val Arg Lys  
465 470 475 480

AAT GGT GTT GCC GCG CCA TCT GCC ACC AGC CAG CTA TCA ACT CGC GCC  
1488  
Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu Ser Thr Arg Ala  
485 490 495

CTG GAA GGG ATT TTT GAA GCA ACT CAT CGA TTG ATT TAC GGC GCT AAG  
1536  
Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile Tyr Gly Ala Lys  
500 505 510

GAT GAC TCT GGT CAG AGA TAC CTG GCC TGG TCT GGA CAC AGT GCC CGT  
1584  
Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly His Ser Ala Arg  
515 520 525

GTC GGA GCC GCG CGA GAT ATG GCC CGC GCT GGA GTT TCA ATA CCG GAG  
1632  
Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val Ser Ile Pro Glu  
530 535 540

ATC ATG CAA GCT GGT GGC TGG ACC AAT GTA AAT ATT GTC ATG AAC TAT  
1680

Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile Val Met Asn Tyr  
545 550 555 560

ATC CGT AAC CTG GAT AGT GAA ACA GGG GCA ATG GTG CGC CTG CTG GAA  
1728

Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val Arg Leu Leu Glu  
565 570 575

GAT GGC GAT TAG

1740

Asp Gly Asp

## FIGURE 26C

SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
1 5 10 15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
20 25 30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
180 185 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
195 200 205

Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
210 215 220

Gly Ser Arg Arg Ala Ser Val Gly Ser His Met Pro Met Ala Asn Leu  
225 230 235 240

Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val Asp Ala Thr Ser  
245 250 255

Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg Asp Arg Gln Ala  
260 265 270

Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val Cys Arg Ser Trp

275

280

285

Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe Pro Ala Glu Pro  
290 295 300

Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala Arg Gly Leu Ala  
305 310 315 320

Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn Met Leu His Arg  
325 330 335

Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala Val Ser Leu Val  
340 345 350

Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly Glu Arg Ala Lys  
355 360 365

Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln Val Arg Ser Leu  
370 375 380

Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn Leu Ala Phe Leu  
385 390 395 400

Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu Ile Ala Arg Ile  
405 410 415

Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg Met Leu Ile His  
420 425 430

Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly Val Glu Lys Ala  
435 440 445

Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp Ile Ser Val Ser  
450 455 460

Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys Arg Val Arg Lys  
465 470 475 480

Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu Ser Thr Arg Ala  
485 490 495

Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile Tyr Gly Ala Lys  
500 505 510

Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly His Ser Ala Arg  
515 520 525

Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val Ser Ile Pro Glu  
530 535 540

Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile Val Met Asn Tyr  
545 550 555 560

Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val Arg Leu Leu Glu  
565 570 575

Asp Gly Asp